AMENDMENT

Please amend the subject application as follows:

IN THE CLAIMS:

1-27. (Canceled)

28. (New) A method for determining the likelihood that a human patient suspected of SMEI does or does not have SMEI comprising:

(1) screening a patient sample for the existence of a mutation in the SCN1A gene of the patient, including in a regulatory region of the gene, by sequencing the SCN1A gene;

(2) identifying the mutation; and

(3) ascertaining whether the mutation, when one is detected, has previously been detected in a patient clinically diagnosed with SMEI and is therefore considered SMEI associated or has previously been detected in a patient unaffected by SMEI and is therefore considered non-SMEI associated, or if not considered to be either, (i) considering genetic data for the parents of the patient and establishing whether the mutation has arisen *de novo* or is inherited; and (ii) establishing whether the mutation is a truncating mutation; wherein

(a) the patient is categorized as having a high probability of having SMEI when the mutation is SMEI associated, wherein the SMEI associated mutation is the presence of a G nucleotide in the SCN1A gene at a position corresponding to position 517 of SEQ ID NO: 1;

(b) the patient is categorized as having a low probability of having SMEI when the mutation is non-SMEI associated; or

(c) the patient is categorized as having a low probability of SMEI in the case of an inherited mutation, a high probability of SMEI in the case

of a *de novo* mutation, and a very high probability of SMEI in the case of a *de novo* mutation which is truncating.

29. (New) The method of claim 28, further comprising identifying one of the SMEI associated SCN1A gene mutations selected from the group consisting of: c301C→T; c512T→A; c596C→G; c677C→T; c715G→A; c2837G→A; c3714A→C; c4186T→G; c4321G→C; c4633A→G; c4934G→A; c5119T→G; c5347G→A; c41delT; c496insGTGAATC; c1687delC; c3231delA; c3561-3562delAA; c4062delT; c4526delA; c3022G→T; c4279C→T; IVS4+5G→A; and IVS3-13T→A.

30. (New) The method of claim 28, wherein the non-SMEI associated mutation in the SCN1A gene is selected from the group consisting of: c580G→A; c4439G→T; c4907G→A; c1724delT; and c5741-5742delAA.